WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising a polymorphic site selected from the group consisting of positions 164, 269, 284, 407 and 989 of SEQ ID NO: 1 and at least 17 contiguous bases of SEQ ID NO: 1 adjacent to the polymorphic site, wherein the nucleic acid molecule comprises

i) an adenine base at position 164 of SEQ ID NO: 1;

ii) a guanine base at position 164 of SEQ ID NO: 1;

iii) a cytosine base at position 269 of SEQ ID NO: 1;

iv) a thymine base at position 269 of SEQ ID NO: 1;

v) a guanine base at position 284 of SEQ ID NO: 1;

vi) a thymine base at position 284 of SEQ ID NO: 1;

vii) a guanine base at position 407 of SEQ ID NO: 1;

viii) a cytosine base at position 407 of SEQ ID NO: 1;

ix) a cytosine base at position 989 of SEQ ID NO: 1; or

x) a thymine base at position 989 of SEQ ID NO: 1;

or a nucleic acid molecule that is fully complementary to a nucleic acid sequence of (i)-(x), provided that the a nucleic acid molecule is not one consisting of SEQ ID NO: 1.

2. A nucleic acid molecule according to Claim 1, which comprises at least 15 contiguous bases of SEQ ID NO: 1 adjacent to the polymorphic site.

3. A nucleic acid molecule according to Claim 1, which comprises at least 20 contiguous bases of SEQ ID NO: 1 adjacent to the polymorphic site.

4. An isolated nucleic acid molecule according to Claim 1, which comprises not more than 150 nt.

5. An isolated nucleic acid molecule according to Claim 1, which comprises not more than 100 nt.

6. An isolated nucleic acid molecule according to Claim 1, which comprises not more than 50 nt.

7. A nucleic acid molecule according to Claim 1, wherein the polymorphic site is within 4 nucleotides of the center of the nucleic acid molecule.

8. A nucleic acid molecule according to Claim 7, wherein the polymorphic site is at the center of the nucleic acid molecule.

9. A nucleic acid molecule according to Claim 1, wherein the polymorphic site is at the 3'-end of the nucleic acid molecule.

10. An array of nucleic acid molecules comprising at least two nucleic acid molecules according to Claim 8.

11. A kit comprising a nucleic acid molecule of Claim 1, and a suitable container.

12. A method for detecting single nucleotide polymorphism (SNP) in bovine proteinase inhibitor (PI) gene, wherein the PI gene have a nucleic acid sequence of SEQ ID NO: 1, the method comprising determining the identity of a nucleotide at position 164, 269, 284, 407 or 989, and comparing the identity to the nucleotide identity at a corresponding position of SEQ ID NO: 1.

13. A method according to Claim 12, wherein the identity of at least two positions of positions 164, 269, 284, 407 and 989 are determined.

14. A method according to Claim 12, wherein the identity of all of positions 164, 269, 284, 407 and 989 are determined.

15. A method for haplotyping a bovine cell, comprising determining the identity of the nucleotides of at least two positions of 164, 269, 284, 407 and 989 of bovine PI gene having a sequence of SEQ ID NO: 1, and comparing the identities at the respective positions to that shown in the table below:

POSITION	164	269	284	407	989
Wild type	G	C	G	G	C
Haplotype 1 (ACGCT)	A	C	G	C	T
Haplotype 2 (GTTGT)	G	T	T	G	T
Haplotype 3 (GCGGT)	G	C	G	G	T
Haplotype 4 (GTTGC)	G	T	T	G	C
Haplotype 5 (GCGGC)	G	C	G	G	C
Haplotype 6 (ACGCC)	A	C	G	C	C

thereby determining the haplotype.

16. A method according to Claim 15, wherein the bovine cell is an adult cell, an embryo cell, a sperm, an egg, a fertilized egg, or a zygote.

17. A method according to Claim 15, wherein the identity of the nucleotide is determined by sequencing the PI gene, or a relevant fragment thereof, isolated from the cell.

18. A method according to Claim 17, wherein the PI gene or a relevant fragment thereof is isolated from the cell via amplification by the polymerase chain reaction (PCR) of genomic DNA of the cell, or by RT-PCR of the mRNA of the cell.

19. A method according to Claim 17, wherein the PCR or RT-PCR is conducted with a pair of primers selected from the group consisting of (1) SEQ ID NO: 2 and SEQ ID NO: 3; and (2) SEQ ID NO: 4 and SEQ ID NO: 5.

20. A method according to Claim 17, wherein both copies of the PI gene in the cell are haplotyped.

21. A method for progeny testing of cattle, the method comprising collecting a nucleic acid sample from said progeny, and haplotyping said nucleic sample according to Claim 15.

22. A method for selectively breeding of cattle using a multiple ovulation and embryo transfer procedure (MOET), the method comprising superovulating a female animal, collecting eggs from said superovulated female, *in vitro* fertilizing said eggs from a suitable male animal, implanting said fertilized eggs into other females allowing for an embryo to develop, and haplotyping said developing embryo according to Claim 15, and terminating pregnancy if said developing embryo is not haplotype 1, 3, 4 or 5.

23. A method according to Claim 22, wherein pregnancy is terminated is said embryo is not haplotype 1.

24. A method for selectively breeding dairy cattles, comprising selecting a bull that is homozygously haplotype 1 and using its semen for fertilizing a female animal.

25. A method according to Claim 24, wherein the female animal is in vitro fertilized.

26. A method according to Claim 24, wherein MOET procedure is used.

27. A method according to Claim 24, wherein said female animal is also homozygously haplotype 1.

28. A method for testing a dairy cattle for its milk production trait, comprising haplotyping its cells according to Claim 15, wherein a cattle having haplotype 1,3, 4 or 5 indicates that the cattle has desirable milk production trait.

29. A method according to Claim 28, wherein a cattle having haplotype 1 indicates that the cattle has a desirable milk production, health or reproduction trait.